

Bl #5

PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/763,909

DATE: 06/26/2001
TIME: 08:56:43

Input Set : A:\13005 002001.TXT
Output Set: N:\CRF3\06262001\I763909.raw

ENTERED

4 <110> APPLICANT: Dikstein, Rivka
5 Yamit-Hezi, Ayala
7 <120> TITLE OF INVENTION: A TRANSCRIPTION FACTOR TFIID SUBUNIT,
8 TAFI1105, POLYPEPTIDES, DNA ENCODING THEREFOR AND
9 PHARMACEUTICAL COMPOSITIONS
12 <130> FILE REFERENCE: 13005/002001
14 <140> CURRENT APPLICATION NUMBER: 09/763,909
15 <141> CURRENT FILING DATE: 2001-02-26
17 <160> NUMBER OF SEQ ID NOS: 6
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2558
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <400> SEQUENCE: 1

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28	aggctgcctg	ctcctcagat	agtgcggcgt	aaagccccca	acaccacgac	aatccagttt	120
29	cctgctaatt	tgccagttcc	tccaggaacc	gttttgcatt	aaagtaacag	tggtccgtt	180
30	atgttggat	ctcctcagca	aactgtaaaca	agagccgaga	ccacaagtaa	cataacctca	240
31	aggccagcag	taccagcgaa	tcctcaaaca	gtcaaaatct	gtacagtgcc	gaactctagc	300
32	tcacaattaa	tcaagaaagt	ggcagtgaca	cctgtaaaa	aattggcaca	aataggaact	360
33	actgtggtaa	ccactgttcc	gaagcccttc	tcagttacaat	ctgtggctgt	gccaaccagt	420
34	rgtctgtcaca	gttactcctg	gaaagccatt	gaataactgt	actaccctga	agccttcaag	480
35	tttgggagca	tcatccactc	cttcaaatga	gcccaatctt	aaagcagaga	actcagcagc	540
36	tgttcagatt	aatcttctc	cgacaatgtc	agaaaatgt	aagaaaatgca	agaacttcct	600
37	tgcaatgtta	ataaaaactag	catgttagtgg	atcacagtcc	cctgaaatgg	ggcaaaaatgt	660
38	gaagaagctg	gttggacaac	tttggatgc	aaaaatcgaa	gcagaagaat	ttacttagaa	720
39	actgtatgtt	gaactcaagt	cttcacctca	gcctcacctg	gttcctttc	ttaagaaaag	780
40	cgtgggtgcc	ttacgacaac	ttctgcctaa	ctcccagagc	ttcatccagc	aatgtgttca	840
41	gcagacttct	agtgacatgg	tcattgctac	ctgtactaca	acagtaacaa	cttctcctgt	900
42	ggtgacact	acagtgtcct	caagccagtc	tgaaaagtca	attattgtt	ctggagcaac	960
43	agcacccaga	actgtgtcag	tgc当地actt	gaaccactt	gctggccag	tgggagcaaa	1020
44	agctggagtt	gtgacacttc	attctgtgg	cccaactgt	gcaacaggag	gaacaacagc	1080
45	tggaaactggt	ttgtttccaga	cttcaaaaacc	acttgcata	tctgtggcaa	acacagtgac	1140
46	cacggctctca	ctgcaacctg	aaaagccagt	tgtctctgga	acagcagtaa	cactgtccct	1200
47	tccagcagta	actttttggag	aaacttcag	tgcagttt	tgtcttccat	ctgtgaaacc	1260
48	tgttgggttcc	ttctgtgg	accacatctg	caagccgtt	attgggactc	cagttcaat	1320
49	caaacttgcc	cagccggcc	ctgtcccttc	acaaccagct	gggattccaa	caggcagttc	1380
50	aagaagcaa	ctattctcat	tgtttcacgt	agttcagcag	ccttcaggag	gcaatgaaaa	1440
51	acaagtgacc	acaatttcac	attcctcaac	attgaccatt	cagaatgt	gacagaagac	1500
52	gatgccagt	aacaccataa	tacctactag	tcagttcct	ccagcttcca	ttctaaagca	1560
53	aattacctct	gcctggaaat	aaaattctgt	cacttcaagc	atctcctact	cagaaaaata	1620
54	gaataaaaaga	gaatgtaaaca	tcatgttcc	gagatgagga	tgacatcaat	gatgtgactt	1680
55	ctatggcagg	ggtcaacctt	aatgaagaaa	atgcctgcat	cttagcaaca	aactctgaat	1740
56	tgggtggcac	actcattcag	tcatgtaaag	atgaaccatt	tcttttatt	ggagctctac	1800
57	aaaagagaat	cttagacatt	ggtaaaaagc	atgacattac	agaacttaac	tctgtatgt	1860
58	tgaacttgat	ctcccaagca	acacaggaac	gactacgagg	ccttcttagaa	aaactgactg	1920

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59	caattgctca	gcatcgaaatg	actacttaca	aggcaagtga	aaattacatc	ctgtgttagt	1980										
60	ataccaggc	acagctcaaa	tttcttgaaa	agctggatca	attggagaag	cagagaaagg	2040										
61	atttggaa	aagagaaaatg	ttacttaagg	cagccaagag	tcgttcta	aaagaagatc	2100										
62	cagaacagc	gagattaaag	cagaaagcca	aagaggatca	gcaattggaa	cttgcacaga	2160										
63	tacagcatag	agacgcta	ctcacagctc	ttgcagctat	tggaccaagg	aagaagagac	2220										
64	cactagaatc	tggaatttgc	ggcttaaaag	acaaccttct	tgcttctgg	acatccagcc	2280										
65	tgacagccac	caaacagttg	catcgtaaa	gaatcacgag	aatctgcctc	agggacttga	2340										
66	tattttgat	ggaacaggaa	cgggagatga	agtattctcg	agctctatac	ctggcccttc	2400										
67	tgaagtgacc	actccactct	tccatccaca	tccttgctat	ttactgccaa	agaagacaca	2460										
68	aagcattgtt	gcactgtcct	gaaatttcaa	tttctggaaa	ataacaccaa	catgaaagag	2520										
69	cattgttac	gattagaact	ttattaactc	ttacctat			2558										
71	<210>	SEQ ID NO:	2														
72	<211>	LENGTH:	852														
73	<212>	TYPE:	PRT														
74	<213>	ORGANISM:	Homo sapiens														
76	<400>	SEQUENCE:	2														
77	Gly	Thr	Leu	Val	Thr	Lys	Val	Ala	Pro	Val	Pro	Pro	Lys	Val			
78	1				5			10					15				
79	Ser	Ser	Gly	Pro	Arg	Leu	Pro	Ala	Pro	Gln	Ile	Val	Ala	Val	Lys	Ala	
80						20			25				30				
81	Pro	Asn	Thr	Thr	Thr	Ile	Gln	Phe	Pro	Ala	Asn	Leu	Gln	Leu	Pro	Pro	
82						35			40				45				
83	Gly	Thr	Val	Leu	Ile	Lys	Ser	Asn	Ser	Gly	Pro	Leu	Met	Leu	Val	Ser	
84						50			55				60				
85	Pro	Gln	Gln	Thr	Val	Thr	Arg	Ala	Glu	Thr	Thr	Ser	Asn	Ile	Thr	Ser	
86						65			70				75			80	
87	Arg	Pro	Ala	Val	Pro	Ala	Asn	Pro	Gln	Thr	Val	Lys	Ile	Cys	Thr	Val	
88						85			90				95				
89	Pro	Asn	Ser	Ser	Gln	Leu	Ile	Lys	Lys	Val	Ala	Val	Thr	Pro	Val		
90						100			105				110				
91	Lys	Lys	Leu	Ala	Gln	Ile	Gly	Thr	Thr	Val	Val	Thr	Val	Pro	Lys		
92						115			120				125				
93	Pro	Ser	Ser	Val	Gln	Ser	Val	Ala	Val	Pro	Thr	Ser	Val	Val	Thr	Val	
94						130			135				140				
95	Thr	Pro	Gly	Lys	Pro	Leu	Asn	Thr	Val	Thr	Thr	Leu	Lys	Pro	Ser	Ser	
96						145			150				155			160	
97	Leu	Gly	Ala	Ser	Ser	Thr	Pro	Ser	Asn	Glu	Pro	Asn	Leu	Lys	Ala	Glu	
98						165			170				175				
99	Asn	Ser	Ala	Ala	Val	Gln	Ile	Asn	Leu	Ser	Pro	Thr	Met	Leu	Glu	Asn	
100						180			185				190				
101	Val	Lys	Lys	Cys	Lys	Asn	Phe	Leu	Ala	Met	Leu	Ile	Lys	Leu	Ala	Cys	
102						195			200				205				
103	Ser	Gly	Ser	Gln	Ser	Pro	Glu	Met	Gly	Gln	Asn	Val	Lys	Lys	Leu	Val	
104						210			215				220				
105	Glu	Gln	Leu	Leu	Asp	Ala	Lys	Ile	Glu	Ala	Glu	Glu	Phe	Thr	Arg	Lys	
106						225			230				235			240	
107	Leu	Tyr	Val	Glu	Leu	Lys	Ser	Ser	Pro	Gln	Pro	His	Leu	Val	Pro	Phe	
108						245			250				255				
109	Leu	Lys	Lys	Ser	Val	Val	Ala	Leu	Arg	Gln	Leu	Leu	Pro	Asn	Ser	Gln	

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110	260	265	270	
111	Ser Phe Ile Gln Gln Cys Val Gln Gln Thr Ser Ser Asp	Met Val Ile		
112	275	280	285	
113	Ala Thr Cys Thr Thr Val Thr Thr Ser Pro Val Val Thr Thr			
114	290	295	300	
115	Val Ser Ser Ser Gln Ser Glu Lys Ser Ile Ile Val Ser Gly Ala Thr			
116	305	310	315	320
117	Ala Pro Arg Thr Val Ser Val Gln Thr Leu Asn Pro Leu Ala Gly Pro			
118	325	330	335	
119	Val Gly Ala Lys Ala Gly Val Val Thr Leu His Ser Val Gly Pro Thr			
120	340	345	350	
121	Ala Ala Thr Gly Gly Thr Thr Ala Gly Thr Gly Leu Leu Gln Thr Ser			
122	355	360	365	
123	Lys Pro Leu Val Thr Ser Val Ala Asn Thr Val Thr Thr Val Ser Leu			
124	370	375	380	
125	Gln Pro Glu Lys Pro Val Val Ser Gly Thr Ala Val Thr Leu Ser Leu			
126	385	390	395	400
127	Pro Ala Val Thr Phe Gly Glu Thr Ser Gly Ala Ala Ile Cys Leu Pro			
128	405	410	415	
129	Ser Val Lys Pro Val Val Ser Phe Cys Trp Asp His Ile Cys Lys Pro			
130	420	425	430	
131	Val Ile Gly Thr Pro Val Gln Ile Lys Leu Ala Gln Pro Gly Pro Val			
132	435	440	445	
133	Leu Ser Gln Pro Ala Gly Ile Pro Thr Gly Ser Ser Ser Lys Gln Leu			
134	450	455	460	
135	Phe Ser Leu Phe His Val Val Gln Gln Pro Ser Gly Gly Asn Glu Lys			
136	465	470	475	480
137	Gln Val Thr Thr Ile Ser His Ser Ser Thr Leu Thr Ile Gln Lys Cys			
138	485	490	495	
139	Gly Gln Lys Thr Met Pro Val Asn Thr Ile Ile Pro Thr Ser Gln Phe			
140	500	505	510	
141	Pro Pro Ala Ser Ile Leu Lys Gln Ile Thr Leu Pro Gly Asn Lys Ile			
142	515	520	525	
143	Leu Ser Leu Gln Ala Ser Pro Thr Gln Lys Asn Arg Ile Lys Glu Asn			
144	530	535	540	
145	Val Thr Ser Cys Phe Arg Asp Glu Asp Asp Ile Asn Asp Val Thr Ser			
146	545	550	555	560
147	Met Ala Gly Val Asn Leu Asn Glu Glu Asn Ala Cys Ile Leu Ala Thr			
148	565	570	575	
149	Asn Ser Glu Leu Val Gly Thr Leu Ile Gln Ser Cys Lys Asp Glu Pro			
150	580	585	590	
151	Phe Leu Phe Ile Gly Ala Leu Gln Lys Arg Ile Leu Asp Ile Gly Lys			
152	595	600	605	
153	Lys His Asp Ile Thr Glu Leu Asn Ser Asp Ala Val Asn Leu Ile Ser			
154	610	615	620	
155	Gln Ala Thr Gln Glu Arg Leu Arg Gly Leu Leu Glu Lys Leu Thr Ala			
156	625	630	635	640
157	Ile Ala Gln His Arg Met Thr Thr Tyr Lys Ala Ser Glu Asn Tyr Ile			
158	645	650	655	

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159 Leu Cys Ser Asp Thr Arg Ser Gln Leu Lys Phe Leu Glu Lys Leu Asp
 160 660 665 670
 161 Gln Leu Glu Lys Gln Arg Lys Asp Leu Glu Glu Arg Glu Met Leu Leu
 162 675 680 685
 163 Lys Ala Ala Lys Ser Arg Ser Asn Lys Glu Asp Pro Glu Gln Leu Arg
 164 690 695 700
 165 Leu Lys Gln Lys Ala Lys Glu Leu Gln Gln Leu Glu Leu Ala Gln Ile
 166 705 710 715 720
 167 Gln His Arg Asp Ala Asn Leu Thr Ala Thr Ala Ala Ile Gly Pro Arg
 168 725 730 735
 169 Lys Lys Arg Pro Leu Glu Ser Gly Ile Glu Gly Leu Lys Asp Asn Leu
 170 740 745 750
 171 Leu Ala Ser Gly Thr Ser Ser Leu Thr Ala Thr Lys Gln Leu His Arg
 172 755 760 765
 173 Pro Arg Ile Thr Arg Ile Cys Leu Arg Asp Leu Ile Phe Cys Met Glu
 174 770 775 780
 175 Gln Glu Arg Glu Met Lys Tyr Ser Arg Ala Leu Tyr Leu Ala Leu Leu
 176 785 790 795 800
 177 Lys Glx Pro Leu His Ser Ser Ile His Ile Leu Ala Ile Tyr Cys Gln
 178 805 810 815
 179 Arg Arg His Lys Ala Leu Leu His Cys Pro Glu Ile Ser Ile Ser Gly
 180 820 825 830
 181 Lys Glx His Gln His Glu Arg Ala Leu Phe Thr Ile Arg Thr Leu Leu
 182 835 840 845
 183 Thr Leu Thr Tyr
 184 850
 186 <210> SEQ ID NO: 3
 187 <211> LENGTH: 30
 188 <212> TYPE: DNA
 189 <213> ORGANISM: Artificial Sequence
 191 <220> FEATURE:
 192 <223> OTHER INFORMATION: NFkB Oligonucleotide
 194 <400> SEQUENCE: 3
 195 agcttaggga ctttccgagg ggactttccg 30
 197 <210> SEQ ID NO: 4
 198 <211> LENGTH: 30
 199 <212> TYPE: DNA
 200 <213> ORGANISM: Artificial Sequence
 202 <220> FEATURE:
 203 <223> OTHER INFORMATION: NFkB Oligonucleotide
 205 <400> SEQUENCE: 4
 206 gatccggaaa gtccccctcgaa aagtcctcta 30
 208 <210> SEQ ID NO: 5
 209 <211> LENGTH: 30
 210 <212> TYPE: DNA
 211 <213> ORGANISM: Artificial Sequence
 213 <220> FEATURE:
 214 <223> OTHER INFORMATION: Mutated NFkB Oligonucleotide
 216 <400> SEQUENCE: 5

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217 agcttatcta ctttccgagt ctactttccg 30
219 <210> SEQ ID NO: 6
220 <211> LENGTH: 30
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: Mutated NFkB Oligonucleotide
227 <400> SEQUENCE: 6
228 gatccggaaa gtagactcgaa 30
aaagtagata

VERIFICATION SUMMARY

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Input Set : A:\13005 002001.TXT

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